CLAIMS

What is claimed is:

1. An isolated nucleic acid sequence encoding a polypeptide with isoflavone synthase activity having the amino acid sequence set forth in SEQ ID NO:66 wherein

Xaa_{10} is Phe or Leu
Xaa_{16} is Ser or Leu
Xaa_{23} is Ser or Thr
Xaa_{25} is Ile or Lys
Xaa_{39} is Lys or Arg
Xaa_{48} is Pro or Leu
Xaa_{60} is Pro or Leu
Xaa_{73} is Leu or His
Xaa_{74} is Ser or Tyr
Xaa_{95} is Ala or Thr
Xaa_{96} is Asn or His
Xaa_{102} is Asn or Ser
Xaa_{110} is Ile, Val, or Thr
Xaa_{112} is Arg or His
Xaa_{117} is Asn or Ser
Xaa_{118} is Ser or Leu
Xaa_{121} is Met or Arg
Xaa_{122} is Ala or Val
Xaa_{124} is Phe or Ile
Xaa_{129} is Lys or Arg
Xaa_{147} is Lys or Glu
Xaa_{159} is Leu or Phe
Xaa_{162} is Ala or Val
Xaa_{166} is Ser or Gly
Xaa_{170} is Gln or Arg
Xaa_{175} is Val or Leu
Xaa_{183} is Ala or Thr
Xaa_{187} is Thr or Ile
Xaa_{191} is Met or Val
Xaa_{209} is Phe or Tyr
Xaa_{219} is Arg or Trp
Xaa_{223} is Tyr or His
Xaa_{253} is Gly or Glu
Xaa_{259} is Lys or Glu

Xaa_{263} is Val or Asp
Xaa_{264} is Val, Asp, or Ile
Xaa_{268} is Ala or Val
Xaa_{272} is Phe or Leu
Xaa_{285} is Thr or Met
Xaa_{293} is Glu or Asp
Xaa_{294} is Thr, or Ile
Xaa_{301} is Phe or Leu
Xaa_{306} is Thr or Ile
Xaa_{311} is Val or Glu
Xaa_{312} is Val or Ala
Xaa_{325} is Arg or Lys
Xaa_{328} is Gln or Glu
Xaa_{334} is Val or Ala
Xaa_{342} is Arg or Ile
Xaa_{377} is Thr or Ile
Xaa_{381} is Glu or Gly
Xaa_{385} is Tyr, His, or Cys
Xaa_{387} is Ile or Thr
Xaa_{393} is Val or Ile
Xaa_{394} is Leu or Pro
Xaa_{402} is Arg or Lys
Xaa_{404} is Ser or Pro
Xaa_{413} is Ser or Phe
Xaa_{422} is Glu or Gly
Xaa_{428} is Gly or Arg
Xaa_{429} is Pro or Leu
Xaa_{435} is Gln or Arg
Xaa_{447} is Arg or Gly
Xaa_{453} is Asn, Ser, or Ile
Xaa_{459} is Met or Thr, and
Xaa_{485} is Asp or Gly.

2. An isolated polypeptide sequence of SEQ ID NO: 66 wherein
Xaa_{10} is Phe or Leu
Xaa_{16} is Ser or Leu
Xaa_{23} is Ser or Thr
Xaa_{25} is Ile or Lys
Xaa_{39} is Lys or Arg

Xaa_{48} is Pro or Leu
Xaa_{60} is Pro or Leu
Xaa_{73} is Leu or His
Xaa_{74} is Ser or Tyr
Xaa_{95} is Ala or Thr
Xaa_{96} is Asn or His
Xaa_{102} is Asn or Ser
Xaa_{110} is Ile, Val, or Thr
Xaa_{112} is Arg or His
Xaa_{117} is Asn or Ser
Xaa_{118} is Ser or leu
Xaa_{121} is Met or Arg
Xaa_{122} is Ala or Val
Xaa_{124} is Phe or Ile
Xaa_{129} is Lys or Arg
Xaa_{147} is Lys or Glu
Xaa_{159} is Leu or Phe
Xaa_{162} is Ala or Val
Xaa_{166} is Ser or Gly
Xaa_{170} is Gln or Arg
Xaa_{175} is Val or Leu
Xaa_{183} is Ala or Thr
Xaa_{187} is Thr or Ile
Xaa_{191} is Met or Val
Xaa_{209} is Phe or Tyr
Xaa_{219} is Arg or Trp
Xaa_{223} is Tyr or His
Xaa_{253} is Gly or Glu
Xaa_{259} is Lys or Glu
Xaa_{263} is Val or Asp
Xaa_{264} is Val, Asp, or Ile
Xaa_{268} is Ala or Val
Xaa_{272} is Phe or Leu
Xaa_{285} is Thr or Met
Xaa_{293} is Glu or Asp
Xaa_{294} is Thr, or Ile
Xaa_{301} is Phe or Leu
Xaa_{306} is Thr or Ile

Xaa_{311} is Val or Glu
Xaa_{312} is Val or Ala
Xaa_{325} is Arg or Lys
Xaa_{328} is Gln or Glu
Xaa_{334} is Val or Ala
Xaa_{342} is Arg or Ile
Xaa_{377} is Thr or Ile
Xaa_{381} is Glu or Gly
Xaa_{385} is Tyr, His, or Cys
Xaa_{387} is Ile or Thr
Xaa_{393} is Val or Ile
Xaa_{394} is Leu or Pro
Xaa_{402} is Arg or Lys
Xaa_{404} is Ser or Pro
Xaa_{413} is Ser or Phe
Xaa_{422} is Glu or Gly
Xaa_{428} is Gly or Arg
Xaa_{429} is Pro or Leu
Xaa_{435} is Gln or Arg
Xaa_{447} is Arg or Gly
Xaa_{453} is Asn, Ser, or Ile
Xaa_{459} is Met or Thr, and
Xaa_{485} is Asp or Gly.

3. An isolated nucleic acid sequence encoding a polypeptide with isoflavone synthase activity.

4. An isolated nucleic acid sequence encoding a polypeptide with isoflavone synthase activity wherein the nucleic acid sequence is not the nucleic acid sequence set forth in SEQ ID NO:9.

5. The isolated nucleic acid sequence of Claim 1 at least 85% identical to the nucleic acid set forth in SEQ ID NO:1.

6. The isolated nucleic acid equence of Claim 1 at least 90% identical to the nucleic acid set forth in SEQ ID NO:1.

7. The isolated nucleic acid sequence of Claim 1 wherein the nucleic acid hybridizes to the nucleic acid set forth in SEQ ID NO:1

8. The isolated nucleic acid sequence of Claim 1 wherein the encoded polypeptide comprises an amino acid sequence that is at least 95% identical to the amino acid sequence set forth in SEQ ID NO:2.

9. The isolated nucleic acid sequence of Claim 1 selected from the group consisting of SEQ ID NOs:1, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 47, 54, 56, 58, and 60.

10. The isolated nucleic acid sequence of Claim 1 encoding the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NOs:2, 10, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 48, 55, 57, 59, 61, and 66.

11. A chimeric sequence comprising the nucleic acid sequence of Claim 1 operably linked to suitable regulatory sequences.

12. A transformed host cell comprising the chimeric sequence of Claim 11.

13. The transformed host cell of Claim 12 further comprising a second chimeric sequence comprising a nucleic acid sequence encoding a polypeptide that regulates expression of at least one enzyme of the phenylpropanoid pathway.

14. The transformed host cell of Claim 13 wherein the second chimeric sequence comprises a chimera containing the maize R region between the region encoding the C1 DNA binding domain and the C1 activation domain.

15. The transformed host cell of Claim 12 wherein the host cell is a eukaryotic cell.

16. The eukaryotic cell of Claim 13 wherein the cell is a yeast cell.

17. The eukaryotic cell of Claim 15 wherein the cell is a plant cell.

18. The plant cell of Claim 17 wherein the cell is a soybean cell.

19. The plant cell of Claim 17 wherein the cell is a corn cell.

20. A plant comprising in its genome the chimeric sequence of Claim 11.

21. The plant of Claim 20 further comprising in its genome a second chimeric sequence comprising a nucleic acid sequence encoding a polypeptide that regulates expression of at least one enzyme of the phenylpropanoid pathway.

22. The plant of Claim 20 wherein the plant is a soybean plant.

23. The plant of Claim 20 wherein the plant is a corn plant.

24. A seed from the plant of Claim 20.

25. A seed from the plant of Claim 21.

26. A method of altering the level of expression of isoflavone synthase in a host cell comprising:

(a) transforming a host cell with the chimeric sequence of Claim 11;

(b) optionally transforming the host cell with a second chimeric sequence comprising a nucleic acid sequence encoding a polypeptide that regulates expression of at least one enzyme of the phenylpropanoid pathway; and

(c) growing the transformed host cell produced in step (a) or step (b) under conditions that are suitable for expression of the chimeric sequence

wherein expression of the chimeric sequences result in production of altered levels of isoflavone synthase in the transformed host cell.

27. A method of increasing the amount of an isoflavonoid in a host cell comprising:

(a) transforming a host cell with the chimeric sequence of Claim 11:

(b) optionally transforming the host cell with a second chimeric sequence comprising a nucleic acid sequence encoding a polypeptide that regulates expression of at least one enzyme of the phenylpropanoid pathway; and

(c) growing the transformed host cell produced in step (a) or step (b) under conditions that are suitable for expression of the chimeric sequence

wherein expression of the chimeric sequences results in production of an amount of an isoflavonoid in the transformed host cell that is greater than the amount of the isoflavonoid that is produced in a cell that is not transformed with the chimeric sequence of Claim 11.

28. The method of Claim 26 wherein the isoflavonoid is selected from the group consisting of genestein and daidzein.

29. The method of Claim 26 or Claim 27 wherein the host cell is a eukaryotic cell.

30. The method of Claim 26 or Claim 27 wherein the eukaryotic cell is a yeast cell.

31. The method of Claim 26 or Claim 27 wherein the eukaryotic cell is a plant cell.

32. The method of Claim 31 wherein the plant cell is a soybean cell.

33. The method of Claim 31 wherein the plant cell is a corn cell.

34. A method of producing a plant with increased isoflavonoid content comprising

(a) transforming a plant cell with the chimeric sequence of Claim 11;

(b) optionally transforming the plant cell with a second chimeric sequence comprising a nucleic acid sequence encoding a polypeptide that regulates expression of at least one enzyme of the phenylpropanoid pathway; and

(c) growing the transformed plant cell under conditions that promote the regeneration of a whole plant from the transformed cell

wherein the transformed plant regenerated from the transformed cell produces an amount of an isoflavonoid that is greater than the amount of the isoflavonoid that is produced in a plant that is regenerated from a plant cell that is not transformed with the chimeric sequence of Claim 11.

35. The method of Claim 34 wherein the plant is a soybean plant.

36. The method of Claim 34 wherein the plant is a corn plant.

37. The transgenic plant produced by the method of Claim 34.

38. The transgenic plant of Claim 37 wherein the plant is a soybean plant.

39. The transgenic plant of Claim 37 wherein the plant is a corn plant.

40. A seed from the plant of Claim 37.

41. A method of obtaining a nucleic acid sequence encoding all or a substantial portion of the amino acid sequence encoding a plant isoflavone synthase comprising

(a) probing a cDNA or genomic library with the nucleic acid sequence of Claim 1:

(b) identifying a DNA clone that hybridizes with the nucleic acid sequence of Claim 1;

(c) isolating the DNA clone identified in step (b);

(d) sequencing the cDNA or genomic sequence that comprises the clone isolated in step (c); and

(e) demonstrating the functional expression of isoflavone synthase mediated by the cDNA or genomic sequence sequenced in step (d)

wherein the sequenced nucleic acid sequence encodes all or a substantial portion of the amino acid sequence encoding a plant isoflavone biosynthetic enzyme.

42. A method of obtaining a nucleic acid sequence encoding all or a substantial portion of an amino acid sequence encoding a plant isoflavone synthase comprising:

(a) synthesizing an oligonucleotide primer corresponding to a portion of the sequence set forth in a member of selected from the group consisting of SEQ ID NOs:1, 9, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 47, 54, 56, 58, and 60;

(b) amplifying a cDNA insert present in a cloning vector using the oligonucleotide primer of step (a) and a primer representing sequences of the cloning vector to produce an amplified nucleic acid sequence; and

(c) demonstrating the functional expression of isoflavone synthase mediated by the amplified nucleic acid sequence produced in step (b)

wherein the amplified nucleic acid sequence encodes all or a substantial portion of an amino acid sequence encoding a plant isoflavone synthase.

43. The method of Claim 42 wherin the oligonucleotide primer is selected from the group consisting of SEQ ID NOs:5, 6, 7, 8, 11, 12, 13, 14, 41, 42, 49, 50, and 51.

44. The product of the method of Claim 41.

45. The product of the method of Claim 42.

46. A method of altering the level of isoflavonoids in a cell of Claim 12 comprising exposing said cell to a phenylpropanoid pathway altering agent.

47. The method of Claim 46 wherein said agent is selected from the group consisting of a transcription factor and stress.

48. The method of Claim 47 wherein stress is selected from the group consisting of ultraviolet light, temperature, pressure, and phosphate level.

49. The method of Claim 47 wherein said transcription factor is a maize C1 myb-type transcription factor and a myc-type transcription factor R

50. The method of Claim 47 wherein said transcription factor is a chimera containg the maize R region between the C1 DNA binding domain and the C1 activation domain.